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FIG. 1

ATGACGTCCACCTGCACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCC  
CTCTCCAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGGTTATC  
TTCCTCGCCGCCTCTTTCGTGCGCAACATAGTGCTGGCGCTAGTGTTGCAGCGCAAGCCG  
CAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAACCTCCTCGTCACCGACCTGCTGCAG  
ATTTTCGCTCGTGGCCCCCTGGGTGGTGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAAC  
AGCCACTTCTGCACGGCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAAC  
ACCATTGTCTTGGTGTCACTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCTACCCG  
TCCAAGATGACCCAGCGCCGCGGTACCTGCTCCTCTATGGCACCTGGATTGTGGCCATC  
CTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCAGGCTGCCTTTGATGAGCGCAATGCT  
CTCTGCTCCATGATCTGGGGGGCCAGCCCCAGCTACACTATTCTCAGCGTGGTGTCTCTC  
ATCGTCATTCCACTGATTGTCAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCAAGGAC  
AGGCAGCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCAAGGAC  
TGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAGTTCCAGGATGAGAGT  
GAGTTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGCCAAGGAGGGCAGAATGGAAGCCAAG  
GACGGCAGCCTGAAGGCCAAGGAAGGAAGCACGGGGACCAGTGAGAGTAGTGATAGAGGCC  
AGGGGCAGCGAGGAGGTGAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGT  
AAGGAAGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTTCGCACAGAG  
GTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTTGGTGAAGACGACATC  
AATTTTCAGTGAGGATGACGTCGAGGCAGTGAACATCCCGGAGAGCCTCCACCCAGTCGT  
CGTAACAGCAACAGCAACCTCCTCTGCCCAGGTGCTACCAAGTGCAAAGCTGCTAAAGTG  
ATCTTCATCATCATTTTTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTC  
CTGGCCGTGTGGGTGGATGTCGAAACCCAGGTACCCAGTGGGTGATCACCATAATCATC  
TGGCTTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGCTACATGCACAAGACC  
ATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTTCTTCTGCAAGGAAAAGCCCCGAAA  
GAAGATAGCCACCCAGACCTGCCCCGAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCT  
TCCTACGATTCTGCTACTTTTCCTTGA

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FIG.2

MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP  
QLLQVTNRFI FNLLVTDLLQISLVAPWV VATSVPLFWPLNSHFCTALVSLTHLFAFASVN  
TIVLVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA  
LCSMIWGASPSYTI LSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD  
CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGS LKAKEGSTGTSESSVEA  
RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI  
NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS YVLSLGPYCFLAV  
LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCCKEPPK  
EDSHPDLPGTEGGTEGKIVPSYDSATFP

FIG. 3

GCAACCTGTCTCACGCCCTCTGGCTGTTGCC

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FIG. 4

AGTTAGTTCTAAGGCAAACCTT

FIG. 5

1	MTSTCTNSTR	ESNSSHTCMP	LSKMPISLAH	GIIRSTVLVI	<u>FLAASFVGNI</u>
51	<u>VLALVLQ</u> RKP	QLLQVTNRFI	<u>FNLLVTDLLQ</u>	<u>ISLVAPWVVA</u>	<u>TSVPLEFWPLN</u>
101	<u>SHFCTALVSL</u>	<u>THLFAFASVN</u>	<u>TIVLVSVDRY</u>	LSIIHPLSYP	SKMTQRRGYL
151	<u>LLYGTWIVAI</u>	<u>LQSTPPLYGW</u>	GQAAFDERNA	LCSMIWGASP	SYT <u>ILSVVSF</u>
201	<u>IVIPLIVMIA</u>	<u>CYSVVFCAAR</u>	RQHALLYNVK	RHSLEVRVKD	CVENEDEEGA
251	EKKEEFQDES	EFRRQHEGEV	KAKEGRMEAK	DGSLKAKEGS	TGTSESSVEA
301	RGSEEVRESS	TVASDGSMEG	KEGSTKVEEN	SMKADKGRTE	VNQCSIDLGE
351	DDMEFGEDDI	NFSEDDVEAV	NIPESLPPSR	RNSNSNPPLP	RCYQCKAAKV
401	<u>IFIIIFS</u> YVL	<u>SLGPYCFLAV</u>	LAVWVDVETQ	VPQWVITIII	<u>WLFFLQCCIH</u>
451	<u>PYVYGYMHKT</u>	IKKEIQDMLK	KFFCKEKPPK	EDSHPDLPGT	EGGTEGKIVP
501	SYDSATFP				

[illegible]

FIG. 6A

```

ACM4_CHICK      ~~~~~~MANFTFGDLALDVARMGGLASTPSGLRSTGLTTPGLSPT
YDBM_CAEEL      ~~~~~~MTFRDLLSVSFEGPRPDSSAGGSSAGGGGGSAGGAAPSEG
5H1A_HUMAN      ~~~~~~MTFRDILSVTFEGPRASSSTGGSGAGGGAGTVG...P.EG
5H1A_MOUSE      ~~~~~~
5H1A_FUGRU      ~~~~~~
5HT_LYMST       ~~~~~~
A1AD_HUMAN      ~~~~~~
A1AD_MOUSE      ~~~~~~
Q13675          ~~~~~~
Q13729          ~~~~~~
O60451          ~~~~~~
A1AA_RAT        ~~~~~~
O54913          ~~~~~~
A1AA_BOVIN      ~~~~~~
A1AA_CANFA      ~~~~~~
A1AA_RABIT      ~~~~~~
A1AA_HUMAN      ~~~~~~
A1AA_ORYLA      ~~~~~~
O96716          ~~~~~~
O75963          ~~~~~~
HGPRBM8         ~~~~~~

ACM4_CHICK      ~~~~~~MHNLSAQPWQAKMANITYDNVTLSN
YDBM_CAEEL      ~~~~~~MCFAEKGEAGEDVDHHS LFC.P.KKLVGNL...KGFIRN
5H1A_HUMAN      ~~~~~~MDV..LSPGQ...GNNTT...SPPAPFETGGN
5H1A_MOUSE      ~~~~~~MDM..FSLGQ...GNNTT...TSLEPFGTGGN
5H1A_FUGRU      ~~~~~~MDLRATSSND...SNATSGYSDTAAMDWDEGEN
5HT_LYMST       ~~~~~~GLVTSDFNDSYGLT.GQFINGSHSSRSRDNASANDTSATN
A1AD_HUMAN      ~~~~~~PAVGGVPGGAGGGGGVVGAGSGEDNRSSAGEPGSAGAGGD
A1AD_MOUSE      ~~~~~~PAVGGVP.GATGGS AVVGTGSGEDNQSS TAEAGAA.ASGE
Q13675          ~~~~~~MVFLSGNASDS
Q13729          ~~~~~~MVFLSGNASDS
O60451          ~~~~~~MVFLSGNASDS
A1AA_RAT        ~~~~~~MVLLSENASEG
O54913          ~~~~~~MVLLSENASEG
A1AA_BOVIN      ~~~~~~MVFLSGNASDS
A1AA_CANFA      ~~~~~~MVFLSGNASDS
A1AA_RABIT      ~~~~~~MVFLSGNASDS
A1AA_HUMAN      ~~~~~~MVFLSGNASDS
A1AA_ORYLA      ~~~~~~MTPSSVTLNC
O96716          ~~~~~~MSANTTVSPTETTANLTANSTEA
O75963          ~~~~~~MSLNSSL
HGPRBM8         ~~~~~~MTSTCTNSTRESN

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FIG. 6C

ACM4_CHICK	IKGYWPLGAVVCDLWLALDYVVSNASVMNLLTISFD	DRYFC
YDBM_CAEEL	IAGEWVFPDALCEVFVSADILCSTASIWNLSTVGL	DRYWA
5H1A_HUMAN	VLNKWTLGQVTCDFIALDVLCTSSILHLCAIAL	DRYWA
5H1A_MOUSE	VLNKWTLGQVTCDFIALDVLCTSSILHLCAIAL	DRYWA
5H1A_FUGRU	VLNKWTLGQDICDFIALDVLCTSSILHLCAIAL	DRYWA
5HT_LYMST	ISKVWFLHSEVCDMWISVDVLCCTASILHLVAIAM	DRYWA
A1AD_HUMAN	VLGEWAFGRAFCDYWAAVDVLCCTASILSLCTISV	DRYVG
A1AD_MOUSE	VLGEWPFGRTECDYWAAVDVLCCTASILSLCTISV	DRYVG
Q13675	VLGYWAFGRVFCNTWAAVDVLCCTASIMGLCTIS	DRYIG
Q13729	VLGYWAFGRVFCNTWAAVDVLCCTASIMGLCTIS	DRYIG
O60451	VLGYWAFGRVFCNTWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_RAT	ILGYWAFGRVFCNTWAAVDVLCCTASIMGLCTIS	DRYIG
O54913	ILGYWAFGRVFCNTWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_BOVIN	ILGYWAFGRVFCNTWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_CANFA	ILGYWAFGRVFCNTWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_RABIT	ILGYWAFGRVFCNTWAAVDVLCCTASITSLCVIS	DRYIG
A1AA_HUMAN	VLGYWAFGRVFCNTWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_ORYLA	ILDRWVFGVFCNTWAAVDVLCCTASIMSLCVISV	DRYIG
O96716	ILGYWPFGG.YCDVWVSEFDVLNSTASILNLVVI	AFDRFLA
O75963	IRREWIEGVVWCNFSALLYLLISSASMITLGVIA	DRYYA
HGPRBMY8	VPLEWPLNSHFCTALVSTHLFAFASVNTIVLVSV	DRYLS

ACM4_CHICK	VTKPLTYPARRTTKMAGLMTAAAWILSFILWAPAL	.LEFW.
YDBM_CAEEL	ITSPVAYMSKRNKRTAGIMILSVWISSALISLAPL	.LGWK
5H1A_HUMAN	ITDPTIDYVNKRTPRRAAALISLTWLTGFLISIPPM	.LGW.
5H1A_MOUSE	ITDPTIDYVNKRTPRRAAALISLTWLTGFLISIPPM	.LGW.
5H1A_FUGRU	ITDPTIDYVNKRTPRRAAVLISVTWLTGFSISIPPM	.LGW.
5HT_LYMST	VTS.IIDYIRRRSARRILIMIMVWIVAFISIPPL	.FGW.
A1AD_HUMAN	VRHSLKYPAIMTERKAAAILALLWVVALVSVVGPL	.LGW.
A1AD_MOUSE	VRHSLKYPAIMTERKAAAILALLWVVALVSVVGPL	.LGW.
Q13675	VSYPTRYPTIVTQRRGLMALLCVWALSIVISIGPL	.FGW.
Q13729	VSYPTRYPTIVTQRRGLMALLCVWALSIVISIGPL	.FGW.
O60451	VSYPTRYPTIVTQRRGLMALLCVWALSIVISIGPL	.FGW.
A1AA_RAT	VSYPTRYPTIVTQRRGVRALLCVWVLSIVISIGPL	.FGW.
O54913	VSYPTRYPTIVTQRRGVRALLCVWALSIVISIGPL	.FGW.
A1AA_BOVIN	VSYPTRYPTIVTQRRGLMALLCVWALSIVISIGPL	.FGW.
A1AA_CANFA	VSYPTRYPTIVTQRRGLMALLCVWALSIVISIGPL	.FGW.
A1AA_RABIT	VSYPTRYPTIVTQRRGLRALLCVWAFSLVISVGPL	.FGW.
A1AA_HUMAN	VSYPTRYPTIVTQRRGLMALLCVWALSIVISIGPL	.FGW.
A1AA_ORYLA	VSYPTRYPAIMTKRRALLAVMLLWVLSVVISIGPL	.FGW.
O96716	ITAPFTYHTRMTERTAGILLIATVWGLSLVVSFLPI	QAGWY
O75963	VLYPMVYPMKLTGNRAVMALVYIWLHSLIGCLPPL	.FGWS
HGPRBMY8	TIHPLSYPSKMTQRRGYLLYGTWLVATLQSTPPL	.YGWG

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FIG. 6D

ACM4_CHICK	QFIVGKRTVHE.....RECYIQFLSNPAVTFGTATAAFYL
YDBM_CAEEL	QTAQTPNLIYEKNNTVRQC..TFLDLPSYTVYSATGSFFI
5H1A_HUMAN	R.TP.EDRSDPDA.....CTIS..KDHGYTIYSTFGAFYL
5H1A_MOUSE	R.AP.EDRSNPNE.....CTIS..KDHGYTIYSTFGAFYL
5H1A_FUGRU	R.SA.EDRANPDA.....CIIS..QDPGYTIYSTFGAFYL
5HT_LYMST	R.DENNDPDKTGT.....CIIS..QDKGYTIYSTFGAFYL
A1AD_HUMAN	K.EPVPP.....DERFCGIT..EEAGYAVFSSVCSFYI
A1AD_MOUSE	K.EPVPP.....DERFCGIT..EEVGYATFSSVCSFYI
Q13675	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYL
Q13729	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYL
O60451	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYL
A1AA_RAT	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYV
O54913	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYV
A1AA_BOVIN	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYV
A1AA_CANFA	R.QPAPE.....DETTTCQIT..EPPGYVLFSAIGSFYV
A1AA_RABIT	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYV
A1AA_HUMAN	R.QPAPE.....DETTTCQIN..EPPGYVLFSAIGSFYL
A1AA_ORYLA	K.EPAPE.....DETVCKIT..EPPGYATFSAVGSFYI
O96716	R.DNQSEELAIYSDPCLCIFT..ASTAYTTIVSSLIISFYI
O75963	S.VEFDEFKWM.....CVAAWH..REPGYTAFWQIWCALF
HGPRBMY8	QA.....AFDERNALCSMIWGASPSYTIILSVVSFIVI

ACM4_CHICK	PVVIMTVLYIHISLA.SRSRVRRHKPESRKERKGSLSFF
YDBM_CAEEL	PTLLMFFVYFKIYQAFAKHRARQIYRQKVIRKHIESTILH
5H1A_HUMAN	PLLMLVLVLYGRIFERA.....ARFRIRKTVKKVEK.....
5H1A_MOUSE	PLLMLVLVLYGRIFERA.....ARFRIRKTVKKVEK.....
5H1A_FUGRU	PLILMLVLVLYGRIFERKA.....ARFRIRKTVKKTEKA.....
5HT_LYMST	PMLVMMIITYIRIWLIV.....ARSRIKDKFQMTKARL...
A1AD_HUMAN	PMAMIVVMYCRVYVV.....A.....RSTTRSL...
A1AD_MOUSE	PMAMIVVMYCRVYVV.....A.....RSTTRSL...
Q13675	PLAIILVMYCRVYVV.....A.....KRESRGL...
Q13729	PLAIILVMYCRVYVV.....A.....KRESRGL...
O60451	PLAIILVMYCRVYVV.....A.....KRESRGL...
A1AA_RAT	PLAIILVMYCRVYVV.....A.....KRESRGL...
O54913	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_BOVIN	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_CANFA	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_RABIT	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_HUMAN	PLAIILVMYCRVYVV.....A.....KRESRGL...
A1AA_ORYLA	PLAIILVMYCRVYVV.....A.....OKESRGL...
O96716	PLLIMLVFYGIIFERKA.....A.....RDQARKI...
O75963	PFLVMLVCYGFIERV.....ARV.....KARKV...
HGPRBMY8	PLIIMTIACYSVVECAARRQHA.LLYNVKRHSLEVRVKDCV

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FIG. 6E

ACM4_CHICK	KAPPVKQNNNN	SPKRAVEVKEEVRNGKVDDQPSAQTEATG
YDBM_CAEEL	EISHVLPTSDEFAKEEEEEEDSESSGQVENGLGNGNDAI.	
5H1A_HUMAN	.....TGADTRHGASPAPQPK..KSVNG.....E..	
5H1A_MOUSE	.....KGAGTSFGTSSAPPPK..KSLNG.....Q..	
5H1A_FUGRU	.....KASDMCLTLSPAVFHK..RA.NG.....D..	
5HT_LYMST	.....KTEETTLVASPKTEYSVVSDCNGCNSPD..	
A1AD_HUMAN	.....EA.....GVKREER..	
A1AD_MOUSE	.....EA.....GIKREP..	
Q13675	.....KS.....GLKTDK..	
Q13729	.....KS.....GLKTDK..	
O60451	.....KS.....GLKTDK..	
A1AA_RAT	.....KS.....GLKTDK..	
O54913	.....KS.....GLKTDK..	
A1AA_BOVIN	.....KS.....GLKTDK..	
A1AA_CANFA	.....KS.....GLKTDK..	
A1AA_RABIT	.....KS.....GLKTDK..	
A1AA_HUMAN	.....KS.....GLKTDK..	
A1AA_ORYLA	.....KE.....GOKIEK..	
O96716	.....NA.....LEG..	
O75963	.....HCGTVVIVEEDAQRTGRKNSSTSTSSSG..	
HGPRBMY8	ENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDG	
ACM4_CHICK	QQEEKETSNESSTVSMQTQTKDKPTTEILPAGQGQSPAHP	
YDBM_CAEEL	.IEEDECEDEDSDEKRDDHTS...MTTVTATVTGPTA.P	
5H1A_HUMAN	..SGSRNWRLGVESKAGGALCANGAVRQGDDGAAL.EVIE	
5H1A_MOUSE	..PGSGDCRRSAENRAVGTPCANGAVRQGEDDATL.EVIE	
5H1A_FUGRU	..AVSAEWKRGYKFKP..SSPCANGAVRHGEEMESL.EVIE	
5HT_LYMST	..STTEKKKRRAPFKSYG..CSPRPERKKNRAKKLPENAN	
A1AD_HUMAN	..GKAS.....EVVL	
A1AD_MOUSE	..GKAS.....EVVL	
Q13675	..SDSE.....QVTL	
Q13729	..SDSE.....QVTL	
O60451	..SDSE.....QVTL	
A1AA_RAT	..SDSE.....QVTL	
O54913	..SDSE.....QVTL	
A1AA_BOVIN	..SDSE.....QVTL	
A1AA_CANFA	..SDSE.....QVTL	
A1AA_RABIT	..SDSE.....QVTL	
A1AA_HUMAN	..SDSE.....QVTL	
A1AA_ORYLA	..SDSE.....QVIL	
O96716	.....	
O75963	..SRRNAFQGVVYSANQCKALITILVVLGAFMVTWGPYM	
HGPRBMY8	SLKAKEGSTGTSESSVEARGSEEVRESSTVASDGSMEGKE	



FIG. 6F

```

ACM4_CHICK      RVNPTSKWSKIKIVTKQTGTESVTAIEIVPAKAGASDHNS
YDBM_CAEL      YMKREAKISKSVPIEKESAIQKREAKPMRSVMATSYEKVK
5H1A_HUMAN     .VHRVGNsKEHLPL...PSEAGPT...PCAP...ASF
5H1A_MOUSE     .VHRVGNsKGDPL...PSESGAT...SYVP...ACI
5H1A_FUGRU     .VN..SNSKTHLPL...PN...T...P.QS...SSH
5HT_LYMST      GVNSNSSSSERLKQIQIETAEAFAN...GCAEEASTAML
A1AD_HUMAN     RIHC.....RGAAT...GADGAHGMRSA
A1AD_MOUSE     RIHC.....RGAAT...SAKGNPGTOSS
Q13675         RIHR.....KNAPA.....GGSGMASA
Q13729         RIHR.....KNAPA.....GGSGMASA
O60451         RIHR.....KNAPA.....GGSGMASA
A1AA_RAT       RIHR.....KNVPA.....EGGGVSSA
O54913         RIHR.....KNVPA.....EGSGVSSA
A1AA_BOVIN     RIHR.....KNAQV.....CGSGVTSa
A1AA_CANFA     RIHR.....KNAPV.....GGTGVSSA
A1AA_RABIT     RIHR.....KNAPA.....CGSGVASA
A1AA_HUMAN     RIHR.....KNAPA.....CGSGMASA
A1AA_ORYLA     RMHR.....GNTTV.....SEDEAL
O96716         RLEQ.....EN.....NRGKKISLA
O75963         VI...ASEALWGKSSVSPSLETWAT...WLSFASAVCHP
HGPRBMY8       GSTKVEENSMKADKGRTEVNOCSIDLGEDDMEFGEDDINF

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```
ACM4_CHICK      LSNSRPNVARKFASSTARSQVRKKKQMAAR    EKKVTRTTII
YDBM_CAEEL     RHKNRKERIYRK..SLQR...KPKAISAAK...ERRGVKVL
5H1A_HUMAN     ERK..NERN.....AEAKRKMA..LAR...ERKTVKTL
5H1A_MOUSE     ERK..NEPT.....AEAKRKMA..LAR...ERKTVKTL
5H1A_FUGRU     ENI..NEKT.....TGTRRKIA..LAR...ERKTVKTL
5HT_LYMST      ERQCNGGKKISSNDTPYSRTREKLE..LKR...ERKAARTL
A1AD_HUMAN     KG.....HTFRSSLVS....RLLK..FSR..EKKA AKTL
A1AD_MOUSE     KG.....HTLRSSLVS....RLLK..FSR..EKKA AKTL
Q13675         KT.....KT...HF SV.....RLLK..FSR..EKKA AKTL
Q13729         KT.....KT...HF SV.....RLLK..FSR..EKKA AKTL
O60451         KT.....KT...HF SV.....RLLK..FSR..EKKA AKTL
A1AA_RAT       KN.....KT...HF SV.....RLLK..FSR..EKKA AKTL
O54913        KN.....KT...HF SV.....RLLK..FSR..EKKA AKTL
A1AA_BOVIN     KN.....KT...HF SV.....RLLK..FSR..EKKA AKTL
A1AA_CANFA     KN.....KT...HF SV.....RLLK..FSR..EKKA AKTL
A1AA_RABIT     KN.....KT...HF SV.....RLLK..FSR..EKKA AKTL
A1AA_HUMAN     KT.....KT...HF SV.....RLLK..FSR..EKKA AKTL
A1AA_ORYLA     RS.....RT...HFAL.....RLLK..FSR..EKKA AKTL
O96716         K.....K.....K.....K.....EKKAAKTL
O75963         LIYGLWNKT VRKELLGMCFGRYYREFVQ...RORTSRLF
HGPRBMY8       SEDDVEAVNIPE SLPPSRNSNS.NPPLPRCYOCKAAKV
```

ACM4\_CHICK  
YDBM\_CAEEL  
5H1A\_HUMAN  
5H1A\_MOUSE  
5H1A\_FUGRU  
5HT\_LYMST  
A1AD\_HUMAN  
A1AD\_MOUSE  
Q13675  
Q13729  
O60451  
A1AA\_RAT  
O54913  
A1AA\_BOVIN  
A1AA\_CANFA  
A1AA\_RABIT  
A1AA\_HUMAN  
A1AA\_ORYLA  
O96716  
O75963  
HGPRBMY8

ACM4\_CHICK  
YDBM\_CAEEL  
5H1A\_HUMAN  
5H1A\_MOUSE  
5H1A\_FUGRU  
5HT\_LYMST  
A1AD\_HUMAN  
A1AD\_MOUSE  
Q13675  
Q13729  
O60451  
A1AA\_RAT  
O54913  
A1AA\_BOVIN  
A1AA\_CANFA  
A1AA\_RABIT  
A1AA\_HUMAN  
A1AA\_ORYLA  
O96716  
O75963  
HGPRBMY8

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FIG. 6H

ACM4_CHICK	~~~~~
YDBM_CAEEL	V~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~~~~~
A1AD_HUMAN	.RRPLWRVY..GHHWRASTSGTIRQDCAPSSGDAPPGAPLA
A1AD_MOUSE	.R..LW.....PSLRPPLAST..DRRPALRLCPQPAHRT
Q13675	SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
Q13729	SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
O60451	SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
A1AA_RAT	SKH...ALG..YT.LHPPSQAVEGQHRDM.VRIPVGSGET
O54913	SKH...ALG..YT.LHPPSQAVEEQHRGM.VRIPVGSGET
A1AA_BOVIN	SKH...TLG..YT.LHAPSHVLEGGQHKDL.VRIPVGSGET
A1AA_CANFA	~~~~~
A1AA_RABIT	SKH...ALG..YT.LHAPSQAVEGQHKDM.VRIPVGSGET
A1AA_HUMAN	SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
A1AA_ORYLA	AHHHHL SVG..QSQTQGHSLTISLDSKGAPCRLSPSSSVA
O96716	PNHADLNYDPVAMRLKKRGENANGTVNGDANGKANGNIEA
O75963	~~~~~
HGPRBMY8	EDSHPDLPGTEGGTEGKIIVPSYDSATFP~~~~~
ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~~~~~
A1AD_HUMAN	LTALPDPD..PEP...PGTPEMQAPVASRRKPPSA...FR
A1AD_MOUSE	PRGSPSPH..CTPR..PGLRRHAGGAGFGLRPSKASLRLR
Q13675	FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTART
Q13729	FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARG
O60451	FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARR
A1AA_RAT	FYKISKTDGVCEWKFFSSMPQGSARITVSKDQSSACTTARV
O54913	FYKISKTDGVCEWKFFSSMPQGSARITVSKDQSSACTTARV
A1AA_BOVIN	FYKISKTDGVCEWKIFSSLPRGSARMAVARDPSACTTARV
A1AA_CANFA	~~~~~
A1AA_RABIT	FYKISKTDGVCEWKFFSSMPRGSARITVSKDQSSACTTARV
A1AA_HUMAN	FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARV
A1AA_ORYLA	LSRTPSSRDSREWRVFSGGPINSG..PGPTEAGRAKVAKL
O96716	GEGTSSS~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~

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FIG. 6I

ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~~~~~
A1AD_HUMAN	EWRLLGPFRRPTTQLRAKVSSLSHKIRAGGAQRAEAACAQ
A1AD_MOUSE	EWRLLGPLQRPTTQLRAKVSSLSHKFRSGGARRAETACAL
Q13675	KRSRVTRLECS....GMILAHCN..LRLPGSRDSPASASQ
Q13729	HT.PMT~~~~~
O60451	GMDCRYFTKNC....REHIKHVN..FMMPPWRKGLEC~~~
A1AA_RAT	RSKSFLQVCCCV.GSSAPRPEEN..HQVPTIKIHTISLGE
O54913	RSKSFLQVCCCV.GSSTPRPEEN..HQVPTIKIHTISLGE
A1AA_BOVIN	RSKSFLQVCCCL.GPSTPSHGEN..HQIPTIKIHTISLSE
A1AA_CANFA	~~~~~
A1AA_RABIT	RSKSFLQVCCCV.GPSTPNPGEN..HQVPTIKIHTISLSE
A1AA_HUMAN	RSKSFLQVCCCV.GPSTPSLDKN..HQVPTIKVHTISLSE
A1AA_ORYLA	CNKSLHRTCCCILRARTPTQDPAPLGDLPPTIKIHQLSLSE
O96716	~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~
ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~~~~~
A1AD_HUMAN	RSEVEAVSLGVPHEVAEGATCQAYELADYSNLRETDI~~~
A1AD_MOUSE	RSEVEAVSLNVPQDGAEAVICQAYEPGDLSNLRETDI~~~
Q13675	AAGTTGDVPPGRRHQAQLIFVFLVETGFHHVGQDDL DLLT
Q13729	~~~~~
O60451	~~~~~
A1AA_RAT	NGEEV~~~~~
O54913	NGEEV~~~~~
A1AA_BOVIN	NGEEV~~~~~
A1AA_CANFA	~~~~~
A1AA_RABIT	NGEEV~~~~~
A1AA_HUMAN	NGEEV~~~~~
A1AA_ORYLA	KGESV~~~~~
O96716	~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~

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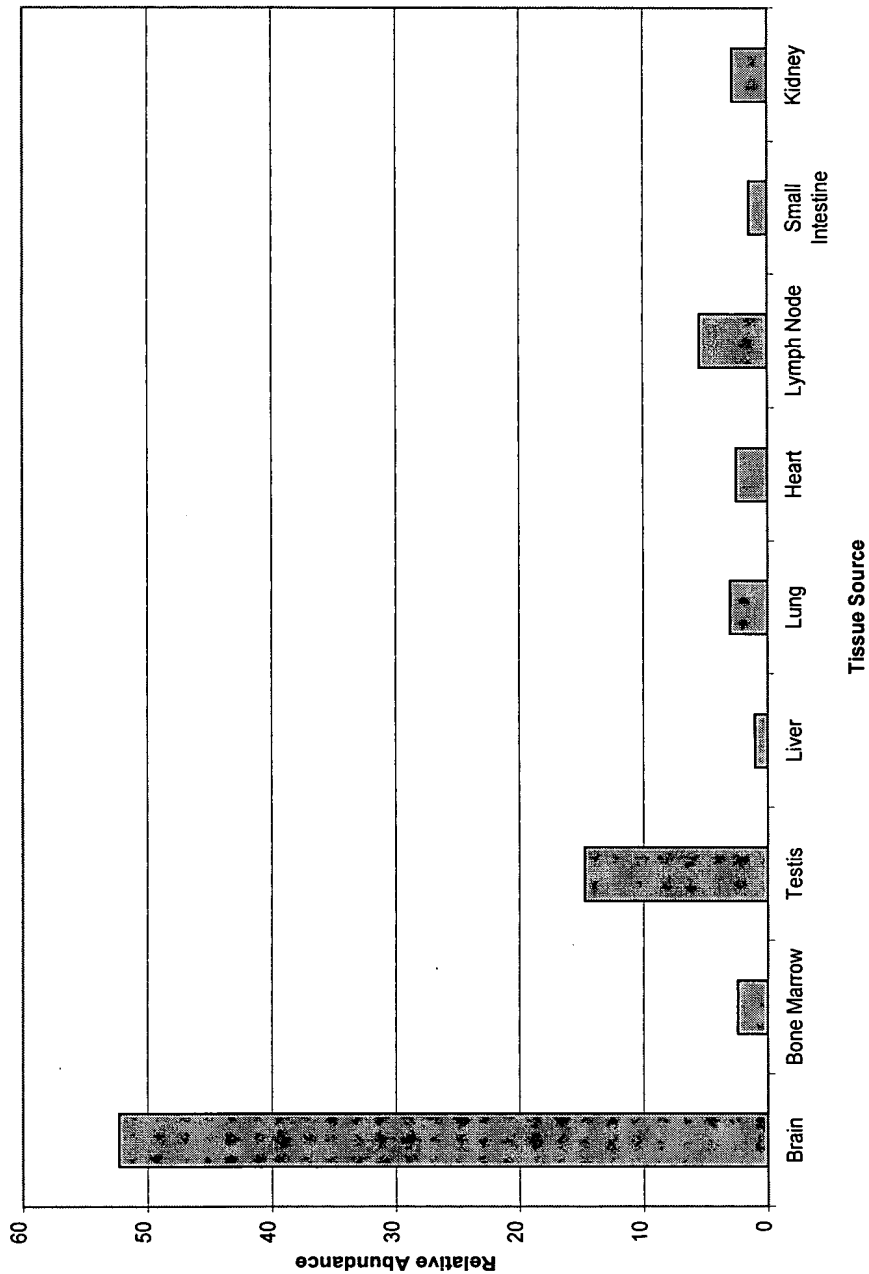
FIG. 6J

ACM4_CHICK	~
YDBM_CAEEL	~
5H1A_HUMAN	~
5H1A_MOUSE	~
5H1A_FUGRU	~
5HT_LYMST	~
A1AD_HUMAN	~
A1AD_MOUSE	~
Q13675	S
Q13729	~
O60451	~
A1AA_RAT	~
O54913	~
A1AA_BOVIN	~
A1AA_CANFA	~
A1AA_RABIT	~
A1AA_HUMAN	~
A1AA_ORYLA	~
O96716	~
O75963	~
HGPRBMY8	~

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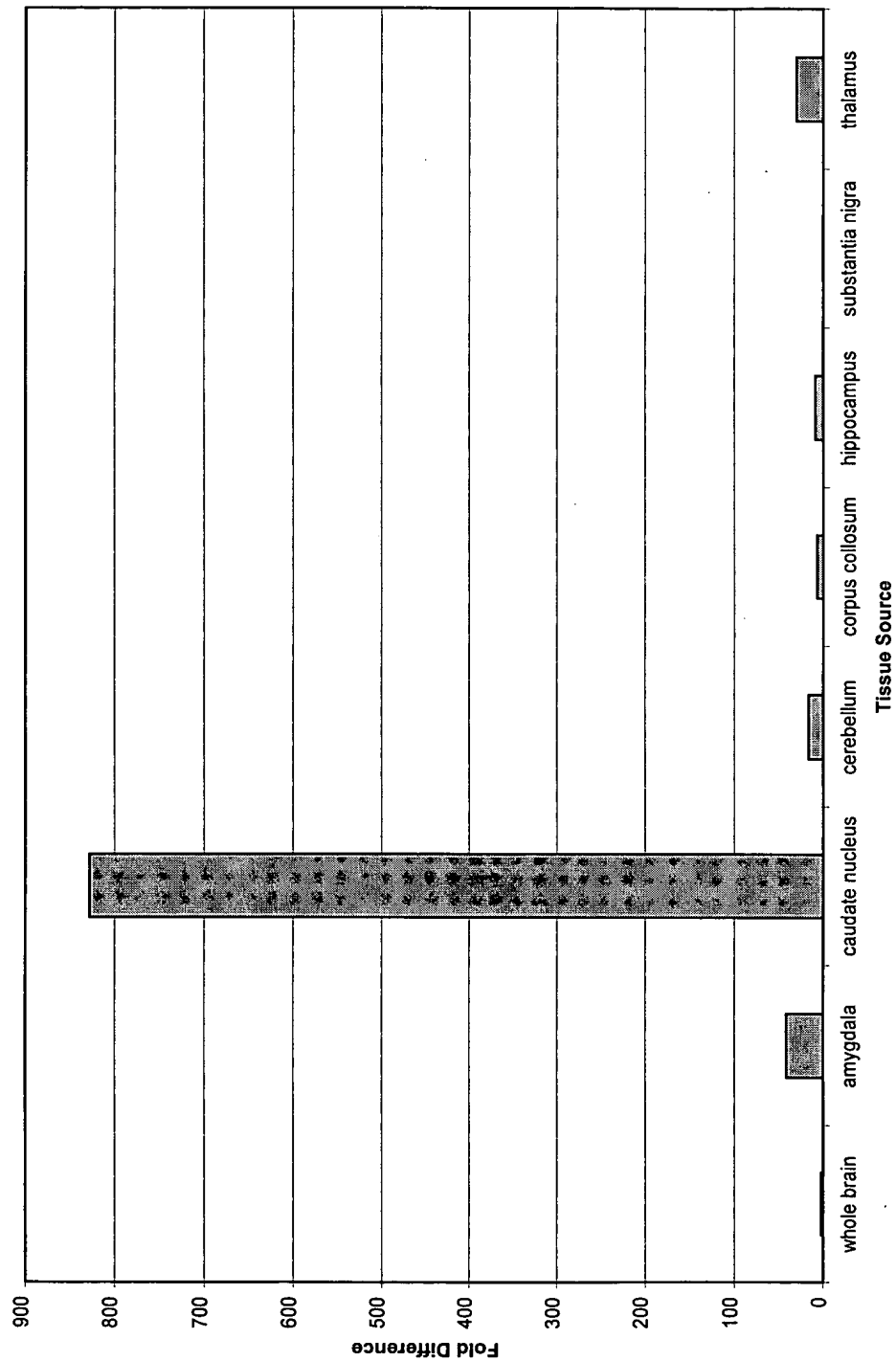
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FIG. 7



D0047 NP

FIG. 8



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FIG. 9

HGPRBMY8 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP  
AL390879 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP  
AX148250 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP  
AX080495 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP

HGPRBMY8 QLLQVTNRFI FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN  
AL390879 QLLQVTNRFI FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN  
AX148250 QLLQVTNRFI FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN  
AX080495 QLLQVTNRFI FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN

HGPRBMY8 TIVVVSVDRLYSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAADFERN  
AL390879 TIVVVSVDRLYSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAADFERN  
AX148250 TIVVVSVDRLYSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAADFERN  
AX080495 TIVVVSVDRLYSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAADFERN

HGPRBMY8 LCSMIWGASPSYTI LSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD  
AL390879 LCSMIWGASPSYTI LSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD  
AX148250 LCSMIWGASPSYTI LSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD  
AX080495 LCSMIWGASPSYTI LSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD

HGPRBMY8 CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGS LKAKEGSTGTSESSVEA  
AL390879 CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGS LKAKEGSTGTSESSVEA  
AX148250 CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGS LKAKEGSTGTSESSVEA  
AX080495 CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGS LKAKEGSTGTSESSVEA

HGPRBMY8 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI  
AL390879 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI  
AX148250 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI  
AX080495 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI

HGPRBMY8 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS YVLSLGPYCFLAV  
AL390879 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS YVLSLGPYCFLAV  
AX148250 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS YVLSLGPYCFLAV  
AX080495 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS YVLSLGPYCFLAV

HGPRBMY8 LAVWVDVETQVPQWVITIIIWLFLLQCCIHYPVYGYMHKTIKKEIQDMLKKFFCCKEPPK  
AL390879 LAVWVDVETQVPQWVITIIIWLFLLQCCIHYPVYGYMHKTIKKEIQDMLKKFFCCKEPPK  
AX148250 LAVWVDVETQVPQWVITIIIWLFLLQCCIHYPVYGYMHKTIKKEIQDMLKKFFCCKEPPK  
AX080495 LAVWVDVETQVPQWVITIIIWLFLLQCCIHYPVYGYMHKTIKKEIQDMLKKFFCCKEPPK

HGPRBMY8 EDSHPDLPGTEGGTEGKIVPSYDSATFP~  
AL390879 EDSHPDLPGTEGGTEGKIVPSYDSATFP\*  
AX148250 EDSHPDLPGTEGGTEGKIVPSYDSATFP\*  
AX080495 EDSHPDLPGTEGGTEGKIVPSYDSATFP\*



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FIG. 10A

AX080495 GCCTGCAACCTGTCTCACGCCCTCTGGCTGTTGCCATGACGTCCACCTGC  
HGPRBMY8 ~~~GCAACCTGTCTCACGCCCTCTGGCTGTTGCCATGACGTCCACCTGC  
AL390879 ~~~~~~ATGACGTCCACCTGC  
AX148250 ~~~~~~ATGACGTCCACCTGC

AX080495 ACCAACAGCAGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC  
HGPRBMY8 ACCAACAGCAGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC  
AL390879 ACCAACAGCAGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC  
AX148250 ACCAACAGCAGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC

AX080495 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG  
HGPRBMY8 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG  
AL390879 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG  
AX148250 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG

AX080495 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG  
HGPRBMY8 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG  
AL390879 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG  
AX148250 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG

AX080495 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA  
HGPRBMY8 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA  
AL390879 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA  
AX148250 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA

AX080495 CCTCCTCGTCACCGACCTGCTGCAGATTTTCGCTCGTGGCCCCCTGGGTGG  
HGPRBMY8 CCTCCTCGTCACCGACCTGCTGCAGATTTTCGCTCGTGGCCCCCTGGGTGG  
AL390879 CCTCCTCGTCACCGACCTGCTGCAGATTTTCGCTCGTGGCCCCCTGGGTGG  
AX148250 CCTCCTCGTCACCGACCTGCTGCAGATTTTCGCTCGTGGCCCCCTGGGTGG

AX080495 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG  
HGPRBMY8 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG  
AL390879 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG  
AX148250 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG

AX080495 GCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT  
HGPRBMY8 GCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT  
AL390879 GCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT  
AX148250 GCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT

AX080495 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT  
HGPRBMY8 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT  
AL390879 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT  
AX148250 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT

AX080495 ACCCGTCCAAGATGACCCAGCGCCGCGTTACCTGCTCCTCTATGGCACC  
HGPRBMY8 ACCCGTCCAAGATGACCCAGCGCCGCGTTACCTGCTCCTCTATGGCACC  
AL390879 ACCCGTCCAAGATGACCCAGCGCCGCGTTACCTGCTCCTCTATGGCACC  
AX148250 ACCCGTCCAAGATGACCCAGCGCCGCGTTACCTGCTCCTCTATGGCACC

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FIG. 10B

AX080495	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
HGPRBMY8	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AL390879	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AX148250	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AX080495	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
HGPRBMY8	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AL390879	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AX148250	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AX080495	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
HGPRBMY8	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AL390879	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AX148250	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AX080495	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
HGPRBMY8	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AL390879	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AX148250	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AX080495	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
HGPRBMY8	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
AL390879	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
AX148250	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
AX080495	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
HGPRBMY8	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AL390879	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AX148250	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AX080495	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
HGPRBMY8	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AL390879	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AX148250	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AX080495	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
HGPRBMY8	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AL390879	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AX148250	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AX080495	GAAGCACGGGGACCACTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
HGPRBMY8	GAAGCACGGGGACCACTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AL390879	GAAGCACGGGGACCACTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AX148250	GAAGCACGGGGACCACTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AX080495	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
HGPRBMY8	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
AL390879	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
AX148250	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA

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FIG. 10C

AX080495	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
HGPRBMY8	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AL390879	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AX148250	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AX080495	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGCGCATGGAGTTT
HGPRBMY8	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AL390879	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AX148250	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AX080495	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
HGPRBMY8	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
AL390879	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
AX148250	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
AX080495	CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCTCCTC
HGPRBMY8	CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCTCCTC
AL390879	CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCTCCTC
AX148250	CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCTCCTC
AX080495	TGCCCAGGTGCTACCAAGTGCAGCTGCTAAAGTGATCTTCATCATCATT
HGPRBMY8	TGCCCAGGTGCTACCAAGTGCAGCTGCTAAAGTGATCTTCATCATCATT
AL390879	TGCCCAGGTGCTACCAAGTGCAGCTGCTAAAGTGATCTTCATCATCATT
AX148250	TGCCCAGGTGCTACCAAGTGCAGCTGCTAAAGTGATCTTCATCATCATT
AX080495	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTCCTGGC
HGPRBMY8	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTCCTGGC
AL390879	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTCCTGGC
AX148250	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTCCTGGC
AX080495	CGTGTGGGTGGATGTGCGAAACCCAGGTACCCAGTGGGTGATCACCATAA
HGPRBMY8	CGTGTGGGTGGATGTGCGAAACCCAGGTACCCAGTGGGTGATCACCATAA
AL390879	CGTGTGGGTGGATGTGCGAAACCCAGGTACCCAGTGGGTGATCACCATAA
AX148250	CGTGTGGGTGGATGTGCGAAACCCAGGTACCCAGTGGGTGATCACCATAA
AX080495	TCATCTGGCTTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
HGPRBMY8	TCATCTGGCTTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AL390879	TCATCTGGCTTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AX148250	TCATCTGGCTTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AX080495	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
HGPRBMY8	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AL390879	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AX148250	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AX080495	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCCG
HGPRBMY8	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCCG
AL390879	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCCG
AX148250	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCCG



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FIG. 11

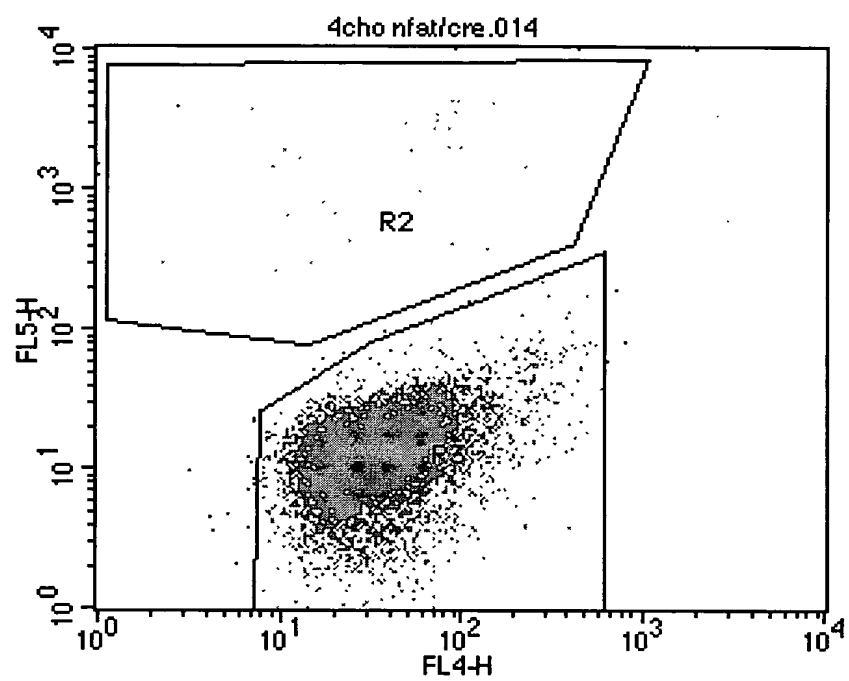


FIG. 12

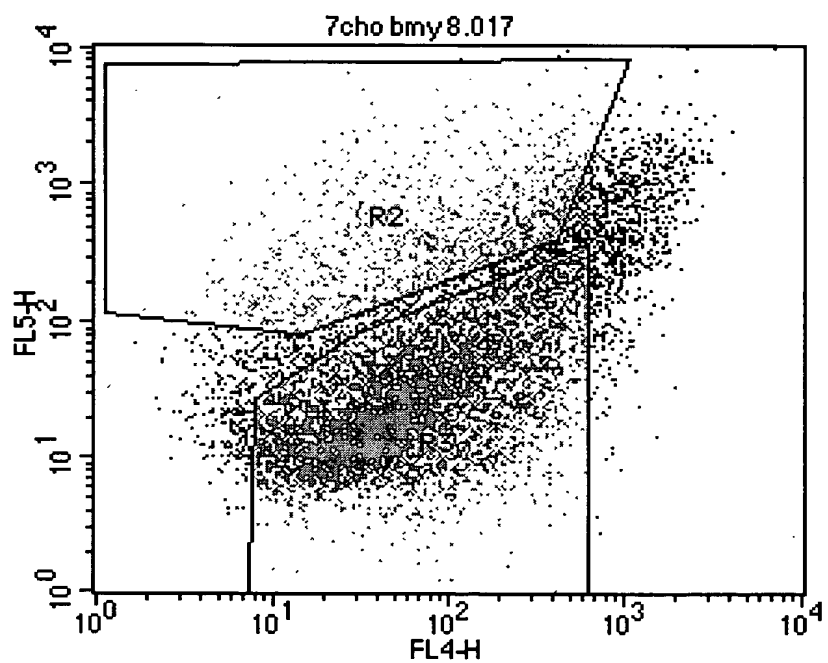


FIG. 13

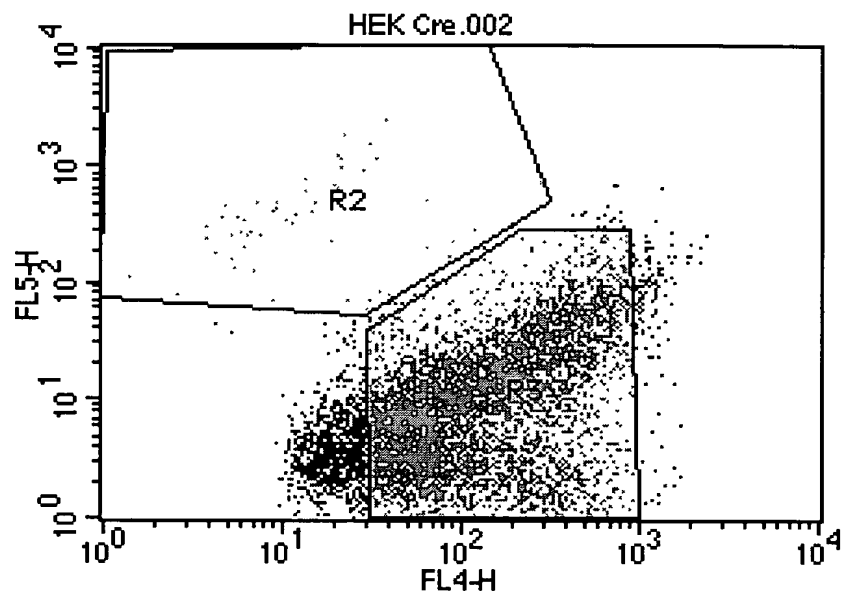


FIG. 14

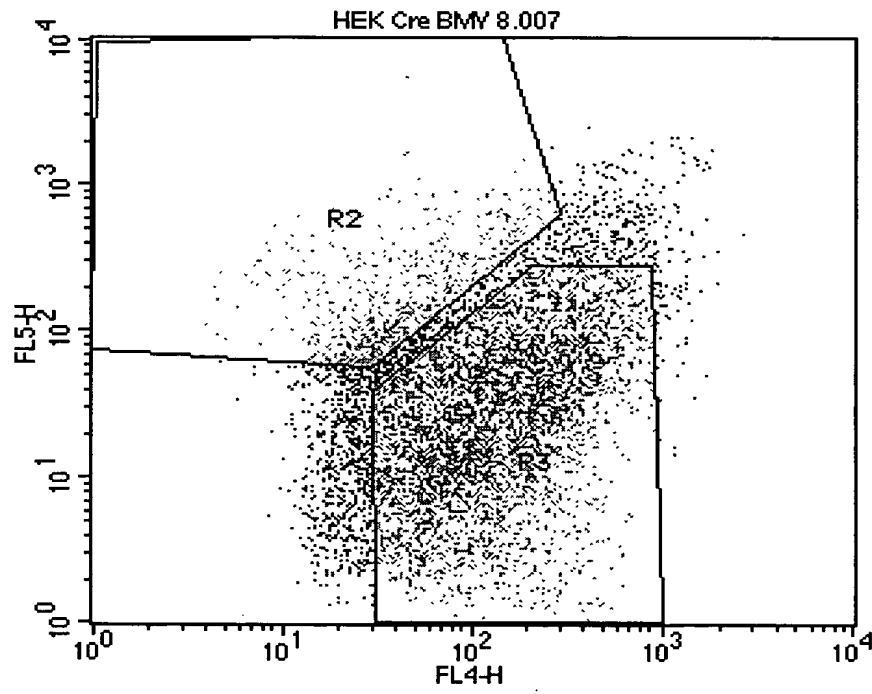
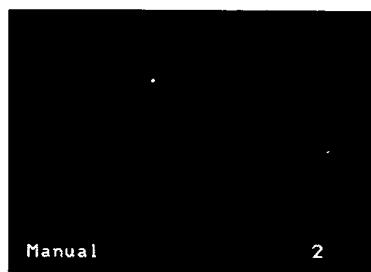


FIG. 15

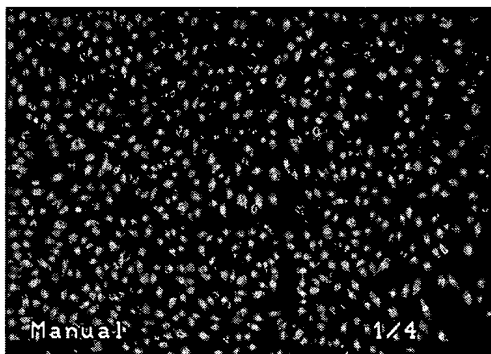
a. CHO-NFAT G alpha 15 (Fluorescent vs. Bright Field)



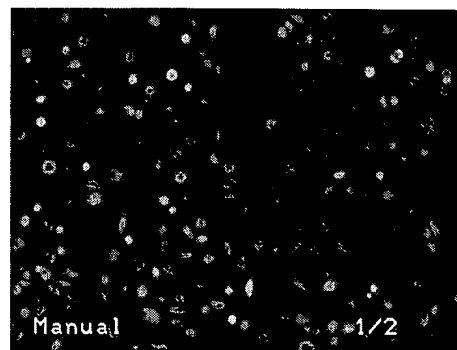
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FIG. 16

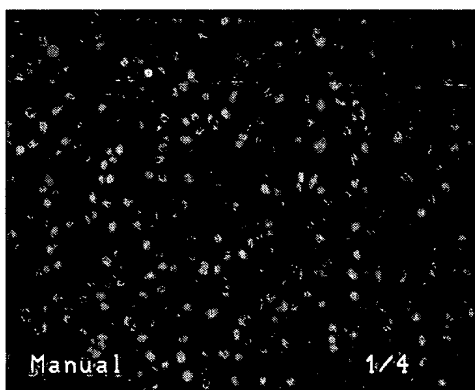
a. CHO-NFAT/CRE



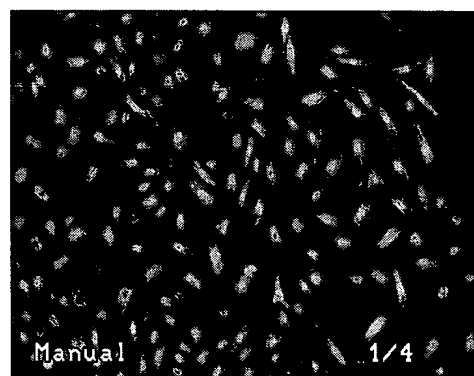
b. CHO-NFAT/CRE + F/T/P



c. CHO-NFAT/CRE oGPCR-Intermediate



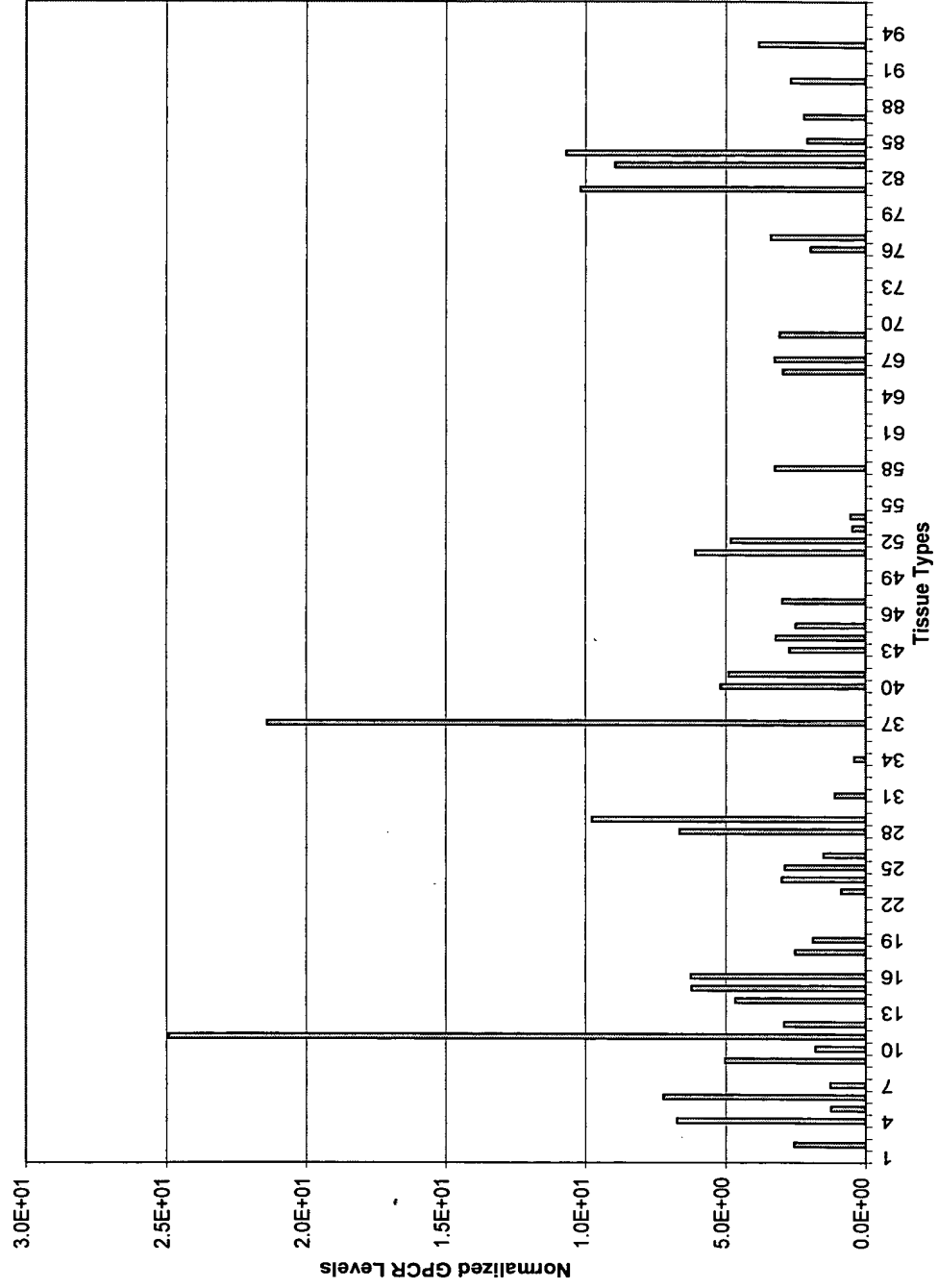
d. CHO-NFAT/CRE oGPCR high





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FIG. 17



[illegible]

FIG. 18A

1	ATGACGTC	CACTGCA	CCCAAC	AGCAGC	CGCGAG	AGAGTA	ACAGCA	GCCACAC	GTGCAT	GGCCC	60										
1	M	T	S	T	C	T	N	S	T	R	E	S	N	S	S	H	T	C	M	P	20
61	CTCTCC	AAAAAT	GGCCAT	CAGCCT	TGGCCC	CACGGC	ATCATC	CGCTCA	ACCGTG	CTGGTT	TATC	120									
21	L	S	K	M	P	I	S	L	A	H	G	I	I	R	S	T	V	L	V	I	40
121	TTCCTC	GGCCGCT	CTTTTC	GTGCGG	CAACAT	AGTGCT	GGCGCT	AGTGTT	GCAGCG	CAAGCCG	180										
41	F	L	A	A	S	F	V	G	N	I	V	L	A	L	V	L	Q	R	K	P	60
181	CAGCTG	CTGCAG	GTGACCA	ACCGT	TTTTAT	CTTTAA	CCCTCCT	CGTCAC	CGACCT	GTGTCAG	240										
61	Q	L	L	Q	V	T	N	R	F	I	F	N	L	L	V	T	D	L	L	Q	80
241	ATTTCG	CTCGTG	GGCCCC	CTGGGT	GGTGGC	CACCTC	TGTGC	CCTCTC	TCTCTG	GGCCCC	TCAAC	300									
81	I	S	L	V	A	P	W	V	V	A	T	S	V	P	L	F	W	P	L	N	100
301	AGCCTT	CTCTGC	ACGGCC	CTGGTT	AGCCTC	ACCCAC	CTGTTG	CGCCTT	CGCCAG	CGTCAAC	360										
101	S	H	F	C	T	A	L	V	S	L	T	H	L	F	A	F	A	S	V	N	120
361	ACCATT	GTCTNT	GGTGTC	AGTGG	ATCGCT	ACTTGT	CCATCAT	CCACC	CTCTCT	CCTACCC	G	420									
121	T	I	V	X	V	S	V	D	R	Y	L	S	I	I	H	P	L	S	Y	P	140
421	TCCAAG	ATGAC	CCAGCG	CGCGGT	TACCTG	CTCCTC	TATGGC	ACCTGG	ATTGTG	GGCCAT	C	480									
141	S	K	M	T	Q	R	R	G	Y	L	L	L	Y	G	T	W	I	V	A	I	160
481	CTGCAG	AGCACT	CCTCCT	CACTCT	ACGGCT	TGGGGC	AGGCTG	CCCTTT	GATGAG	CGCAAT	GC	540									
161	L	Q	S	T	P	P	L	Y	G	W	G	Q	A	A	F	D	E	R	N	A	180
541	CTCTGT	CCATG	ATCTGG	GGGGG	CCAGCC	CCAGCT	ACACTA	TTCTC	AGCGT	GGTGT	CTC	600									
181	L	C	S	M	I	W	G	A	S	P	S	Y	T	I	L	S	V	V	S	F	200
601	ATCGTC	ATTCC	ACTGAT	TGTG	TATG	ATTGC	CTGCTA	CTCCGT	GGTGT	TCTGT	GTCAG	CCCGG	660								
201	I	V	I	P	L	I	V	M	I	A	C	Y	S	V	V	F	C	A	A	R	220
661	AGGCAG	CATGCT	CTGCTG	TACAAT	TGTCA	AGAGAC	ACAGCT	TGGAAG	TGCGAG	TCAAGG	AC	720									
221	R	Q	H	A	L	L	Y	N	V	K	R	H	S	L	E	V	R	V	K	D	240
721	TGTGTG	GAGAAT	GAGGAT	GAAGAG	GGAGC	AGAGA	AAGAAG	GAGGAG	TTCCAG	GATGAG	AGT	780									
241	C	V	E	N	E	D	E	E	G	A	E	K	K	E	E	F	Q	D	E	S	260
781	GAGTTT	CGCCG	CAGCAT	GAAGGT	GAGGT	CAAGGC	CAAGG	AGGGC	AGAATG	GGAAGC	CAAG	840									
261	E	F	R	R	Q	H	E	G	E	V	K	A	K	E	G	R	M	E	A	K	280
841	GACGGC	AGCCTG	AAGGCC	AAGGA	AGGAAG	CACGGG	GACCA	GTGAG	AGTAG	TAGAGG	CCC	900									
281	D	G	S	L	K	A	K	E	G	S	T	G	T	S	E	S	S	V	E	A	300

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FIG. 18B

901 AGGGGCAGCGAGGAGGTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGT 960  
301 R G S E E V R E S S T V A S D G S M E G 320

961 AAGGAAGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCACAGAG 1020  
321 K E G S T K V E E N S M K A D K G R T E 340

1021 GTCAACCAGTGCAGCATTGACTTGGGTGAAGATGNCATGGAGTTTGGTGAAGACGACATC 1080  
341 V N Q C S I D L G E D X M E F G E D D I 360

1081 AATTTTCAGTGAGGATGACGTCGAGGCAGTGAACATCCCGAGAGCCTCCCACCCAGTCGT 1140  
361 N F S E D D V E A V N I P E S L P P S R 380

1141 CGTAACAGCAACAGCAACCCTCCTCTGCCCAGGTGCTACCAGTGCAAAGCTNNNAAAGTG 1200  
381 R N S N S N P P L P R C Y Q C K A X K V 400

1201 ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTC 1260  
401 I F I I I F S Y V L S L G P Y C F L A V 420

1261 CTGGCCGTGTGGGTGGATGTGAAACCCAGGTACCCCAGTGGGTGATCACCATAATCATC 1320  
421 L A V W V D V E T Q V P Q W V I T I I I 440

1321 TGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGCTACATGCACAAGACC 1380  
441 W L F F L Q C C I H P Y V Y G Y M H K T 460

1381 ATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTTCTTCTGCAAGGAAAAGCCCCGAAA 1440  
461 I K K E I Q D M L K K F F C K E K P P K 480

1441 GAAGATAGCCACCCAGACCTGCCCAGAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCT 1500  
481 E D S H P D L P G T E G G T E G K I V P 500

1501 TCCTACGATTCTGCTACTTTTCCTTGA 1527  
501 S Y D S A T F P 508

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